# WEST

## Freeform Search

**Database:** US Patents Full-Text Database
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**Term:** L7 same phosphoramidate

**Display:** 10 **Documents in Display Format:** CIT **Starting with Number** 1

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### Search History

**DATE: Thursday, October 23, 2003** Printable Copy Create Case

| Set Name (side by side) | Query | Hit Count | Set Name (result set) |
|---|---|---|---|
| *DB=USPT; PLUR=YES; OP=OR* | | | |
| L8 | L7 same phosphoramidate | 1 | L8 |
| L7 | Group same I same intron | 471 | L7 |
| L6 | l5 same exon | 1 | L6 |
| L5 | L2 same Group same I | 24 | L5 |
| L4 | L2 same GroupI | 0 | L4 |
| L3 | L2 same oligonucleotide | 1 | L3 |
| L2 | L1 same intron | 36 | L2 |
| L1 | inhibit$ same (self near0 splic$) | 55 | L1 |

END OF SEARCH HISTORY

(FILE 'HOME' ENTERED AT 12:14:46 ON 23 OCT 2003)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE' ENTERED AT 12:15:15 ON 23 OCT 2003
L1 2273 S GROUP(W)I(W)INTRON
L2 229 S L1(P)INHIBIT?
L3 139 S L2 (P)(SELF(W)SPLIC?)
L4 10 S L3(P)PHOSPHORAMIDATE
L5 4 DUPLICATE REMOVE L4 (6 DUPLICATES REMOVED)

=> s l3(p)oligonucleotide
L6 10 L3(P) OLIGONUCLEOTIDE

=> duplicate remove l6
DUPLICATE PREFERENCE IS 'MEDLINE, BIOSIS, CAPLUS, EMBASE'
KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):n
PROCESSING COMPLETED FOR L6
L7 4 DUPLICATE REMOVE L6 (6 DUPLICATES REMOVED)

=> d bib ab l7 1-4

L7 ANSWER 1 OF 4 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2003:432135 CAPLUS
TI Folding and targeting RNA
AU Turner, Douglas; Schroeder, S. J.; Mathews, D. H.; Disney, M. D.; Childs, J. I.
CS University of Rochester, Rochester, NY, USA
SO Abstracts, 31st Northeast Regional Meeting of the American Chemical Society, Saratoga Springs, NY, United States, June 15-18 (2003), 50
Publisher: American Chemical Society, Washington, D. C.
CODEN: 69EBFV
DT Conference; Meeting Abstract
LA English
AB The databases of genome sequences provide a foundation for developing databases of RNA secondary structures. Free energy minimization with nearest neighbor parameters provides useful predictions of possible secondary structures for a given RNA. These predictions depend on free energy parameters for RNA loops. Recent expts. with loops suggest revisions to models used to approx. these free energies. Predictions of secondary structure are improved by simultaneously minimizing free energy and aligning base pairs for two sequences with identical function. Evidently, this combination partially compensates for incomplete knowledge of RNA thermodn. A computer program, called Dynalign, automates this combination of free energy minimization and sequence comparison. Predictions of secondary structure can facilitate design of therapeutics that target RNA. For example, the predicted proclivity of RNA to misfold can be exploited by **oligonucleotide** directed misfolding of RNA (ODMiR) strategies to trap an RNA in a nonfunctional conformation. An application to **inhibition** of **self-splicing** by the **group I intron** from Candida albicans has been demonstrated.

L7 ANSWER 2 OF 4 MEDLINE on STN DUPLICATE 1
AN 2001277619 MEDLINE
DN 21264135 PubMed ID: 11371215
TI Binding enhancement by tertiary interactions and suicide inhibition of a Candida albicans group I intron by phosphoramidate and 2'-O-methyl hexanucleotides.
AU Disney M D; Matray T; Gryaznov S M; Turner D H
CS Departments of Chemistry and Pediatrics, University of Rochester, Rochester, New York 14627-0216, USA.
NC AI45398 (NIAID)
SO BIOCHEMISTRY, (2001 May 29) 40 (21) 6520-6.
Journal code: 0370623. ISSN: 0006-2960.

CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200108
ED Entered STN: 20010820
Last Updated on STN: 20010820
Entered Medline: 20010816
AB Candida albicans is one of many infectious pathogens that are evolving resistance to current treatments. RNAs provide a large class of targets for new therapeutics for fighting these organisms. One strategy for targeting RNAs uses short oligonucleotides that exhibit binding enhancement by tertiary interactions in addition to Watson-Crick pairing. A potential RNA target in C. albicans is the **self-splicing group I intron** in the LSU rRNA precursor. The recognition elements that align the 5' exon splice site for a ribozyme derived from this precursor are complex [Disney, M. D., Haidaris, C. G., and Turner, D. H. (2001) Biochemistry 40, 6507-6519]. These recognition elements have been used to guide design of hexanucleotide mimics of the 5' exon that have backbones modified for nuclease stability. These hexanucleotides bind as much as 100000-fold more tightly to a ribozyme derived from the intron than to a hexanucleotide mimic of the intron's internal guide sequence, r(GGAGGC). Several of these oligonucleotides **inhibit** precursor **self-splicing** via a suicide **inhibition** mechanism. The most promising suicide **inhibitor** is the ribophosphoramidate rn(GCCUC)rU, which forms more trans-spliced than cis-spliced product at **oligonucleotide** concentrations of >100 nM at 1 mM Mg(2+). The results indicate that short oligonucleotides modified for nuclease stability can target catalytic RNAs when the elements of tertiary interactions are complex.

L7 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2000:666925 CAPLUS
DN 133:248036
TI IGS-binding, phosphoramidate- or thiophosphoramidate-linked oligonucleotides for inhibition of Group I intron self-splicing
IN Testa, Stephen M.; Disney, Matthew D.; Gryaznov, Sergei M.; Turner, Douglas H.
PA Geron Corp., USA; University of Rochester
SO PCT Int. Appl., 37 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|---|---|---|---|
| PI WO 2000055374 | A1 | 20000921 | WO 2000-US7045 | 20000315 |

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRAI US 1999-124451P P 19990315
AB A method of **inhibiting** the **self-splicing** of a **Group I intron** is disclosed. The method uses an **oligonucleotide** having a sequence essentially identical to a guide sequence found in the 5' flanking exon and terminates with a 3' ribonucleoside. Usually the **oligonucleotide** has N3'.fwdarw.P5'

phosphoramidate or thiophosphoramidate linkages rather than phosphodiester linkages. A method of **inhibiting** the growth of organisms having **Group I intron**, particularly certain pathogenic fungi including Pneumocystis carinii, Candida albicans and Aspergillus nidulans using the **oligonucleotide** is also provided.

RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 4 OF 4 MEDLINE on STN DUPLICATE 2
AN 2001076965 MEDLINE
DN 20541381 PubMed ID: 11087376
TI Contributions of individual nucleotides to tertiary binding of substrate by a Pneumocystis carinii group I intron.
AU Disney M D; Gryaznov S M; Turner D H
CS Department of Chemistry, University of Rochester, Rochester, New York 14627-0216, USA.
NC AI45398 (NIAID)
SO BIOCHEMISTRY, (2000 Nov 21) 39 (46) 14269-78.
Journal code: 0370623. ISSN: 0006-2960.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200101
ED Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010111
AB Pneumocystis carinii is a mammalian pathogen that infects and kills immunocompromised hosts such as cancer and AIDS patients. The LSU rRNA precursor of P. carinii contains a conserved **group I intron** that is an attractive drug target because humans do not contain group I introns. The **oligonucleotide** r(AUGACU), whose sequence mimics the 3'-end of the 5'-exon, binds to a ribozyme derived from the intron with a K(d) of 5.2 nM, which is 61000-fold tighter than expected from base-pairing alone [Testa, S. M., Haidaris, G. C., Gigliotti, F., and Turner, D. H. (1997) Biochemistry 36, 9379-9385]. Thus, **oligonucleotide** binding is enhanced by tertiary interactions. To localize interactions that give rise to this tertiary stability, binding to the ribozyme has been measured as a function of **oligonucleotide** length and sequence. The results indicate that 4.3 kcal/mol of tertiary stability is due to a G.U pair that forms at the intron's splice junction. Eliminating nucleotides at the 5'-end of r(AUGACU) does not affect intron binding more than expected from differences in base-pairing until r((___)ACU), which binds much more tightly than expected. Adding a C at the 5'- or 3'-end that can potentially form a C-G pair with the target has little effect on binding affinity. Truncated oligonucleotides were tested for their ability to **inhibit** intron **self-splicing** via a suicide **inhibition** mechanism. The tetramer, r((__)GACU), retains similar binding affinity and reactivity as the hexamer, r(AUGACU). Thus oligonucleotides as short as tetramers might serve as therapeutics that can use a suicide **inhibition** mechanism to **inhibit** **self-splicing**. Results with a phosphoramidate tetramer and thiophosphoramidate hexamer indicate that oligonucleotides with backbones stable to nuclease digestion retain favorable binding and reactivity properties.

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**End of Result Set**

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L8: Entry 1 of 1 File: USPT Aug 19, 2003

DOCUMENT-IDENTIFIER: US 6608036 B1
TITLE: Oligonucleotide N3'.fwdarw.P5' thiophosphoramidates: their synthesis and administration to treat neoplasms

Other Reference Publication (12):
Testa, S., et al., "In Vitro Suicide Inhibition of Self-Splicing of a Group I Intron from Pneumocystis Carinii by An N3'.fwdarw.P5' Phosphoramidate Hexanucleotide", Proc. Natl. Acad. Sci. USA, 96:2734 (Mar., 1999).